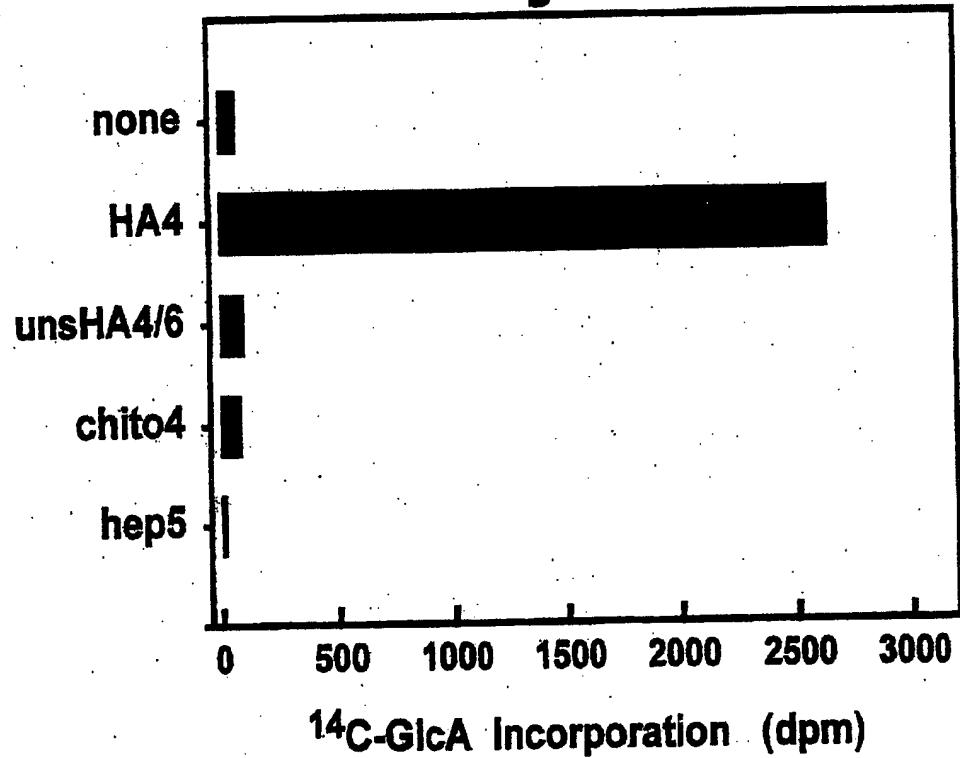
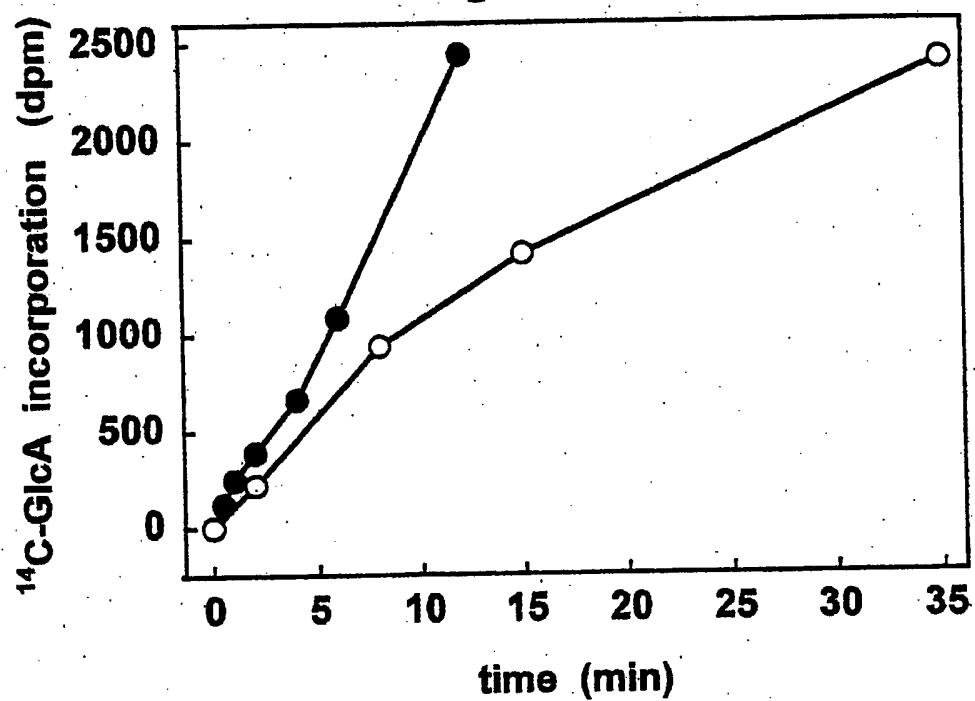
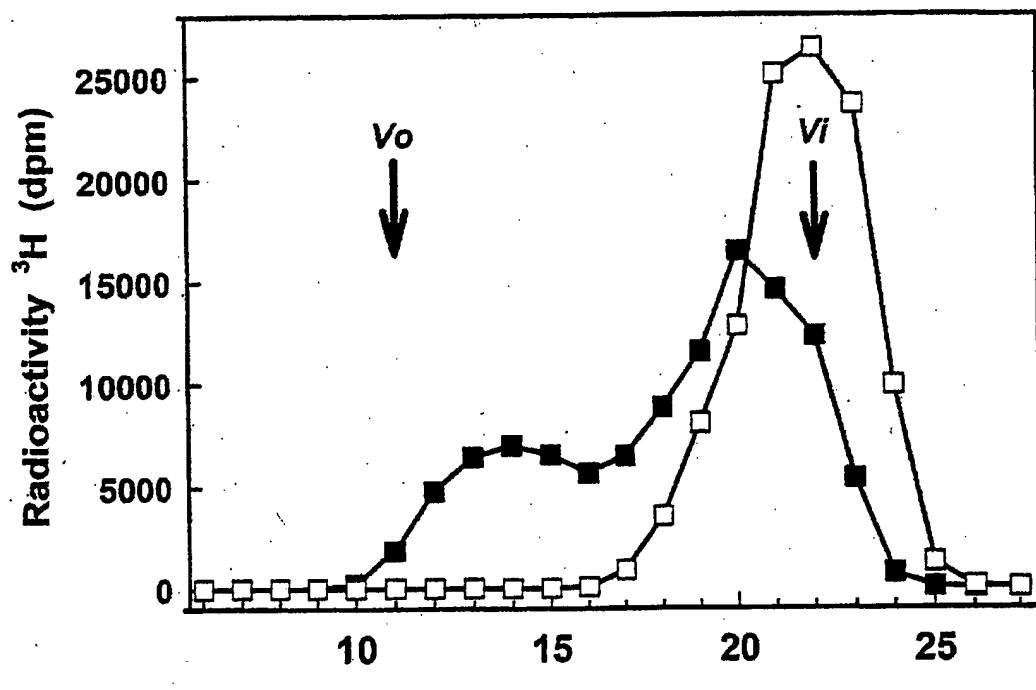


Figure 1



**Figure 2**

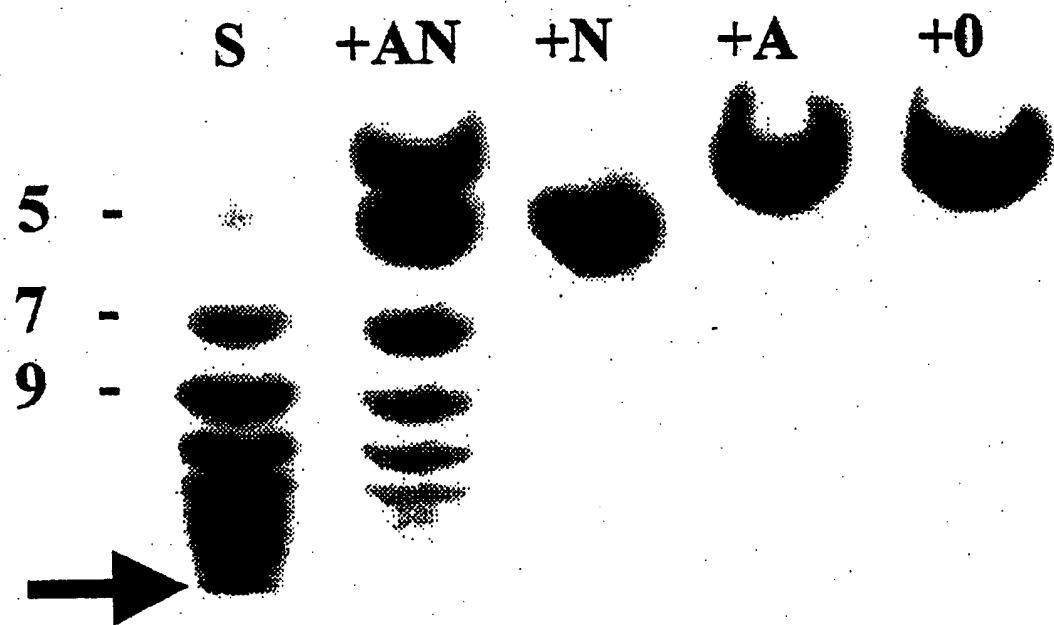




**Figure 3**

Figure 4

HA4 acceptor



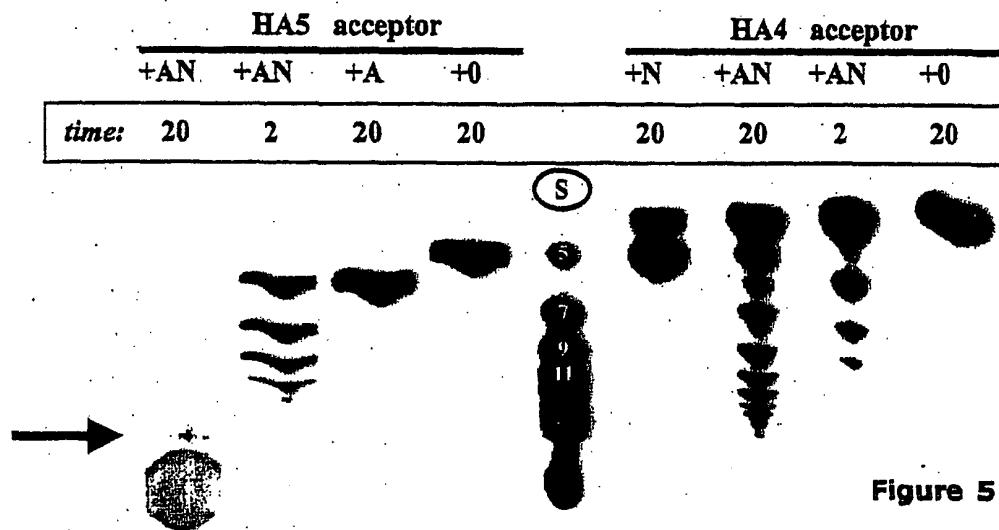


Figure 5

Ion Gel Filtration  
Ex Fractions

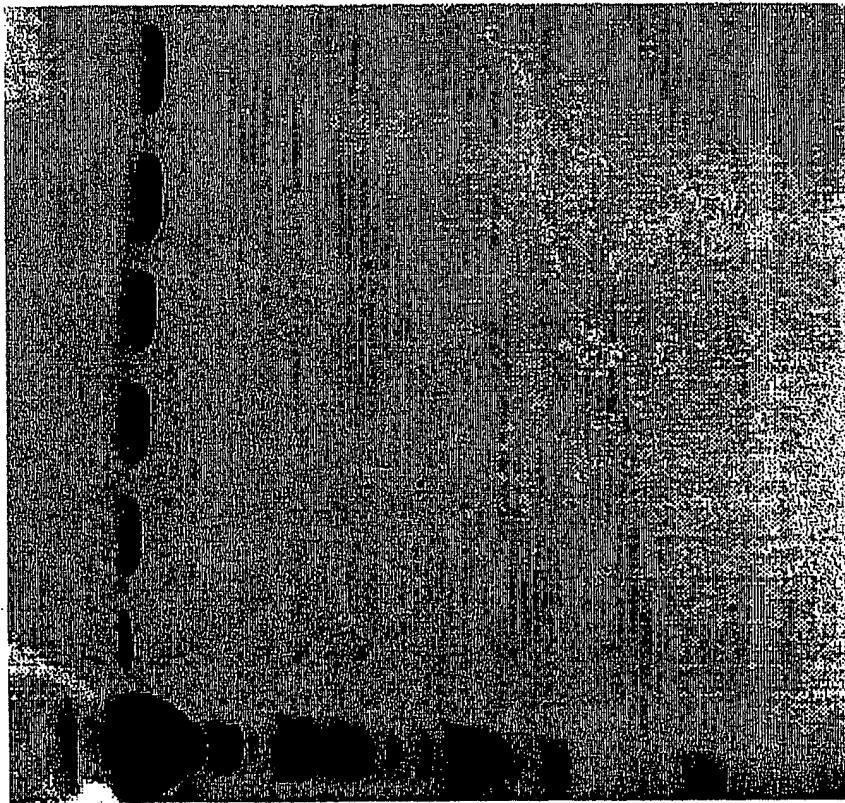
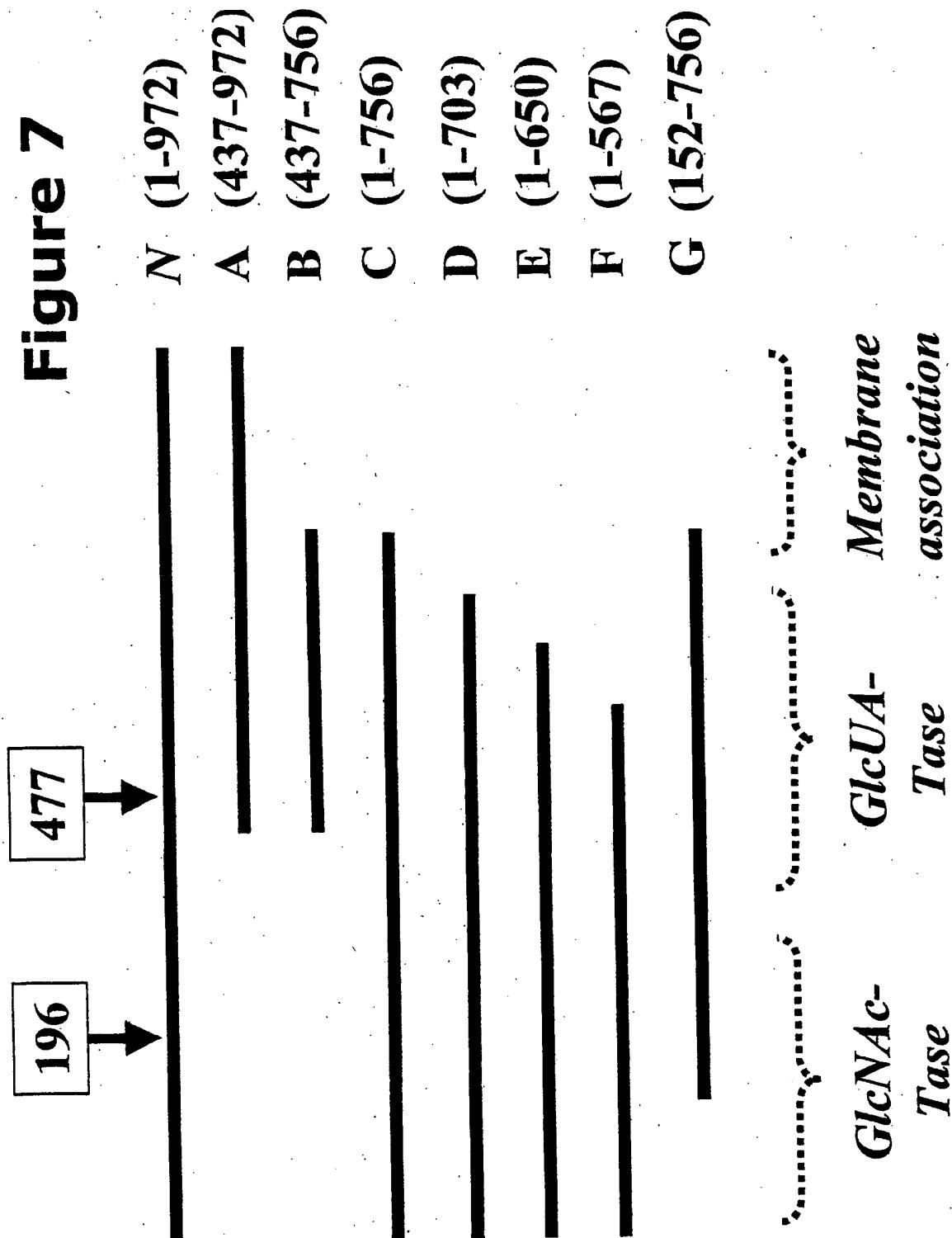


Figure 6

**Figure 7**



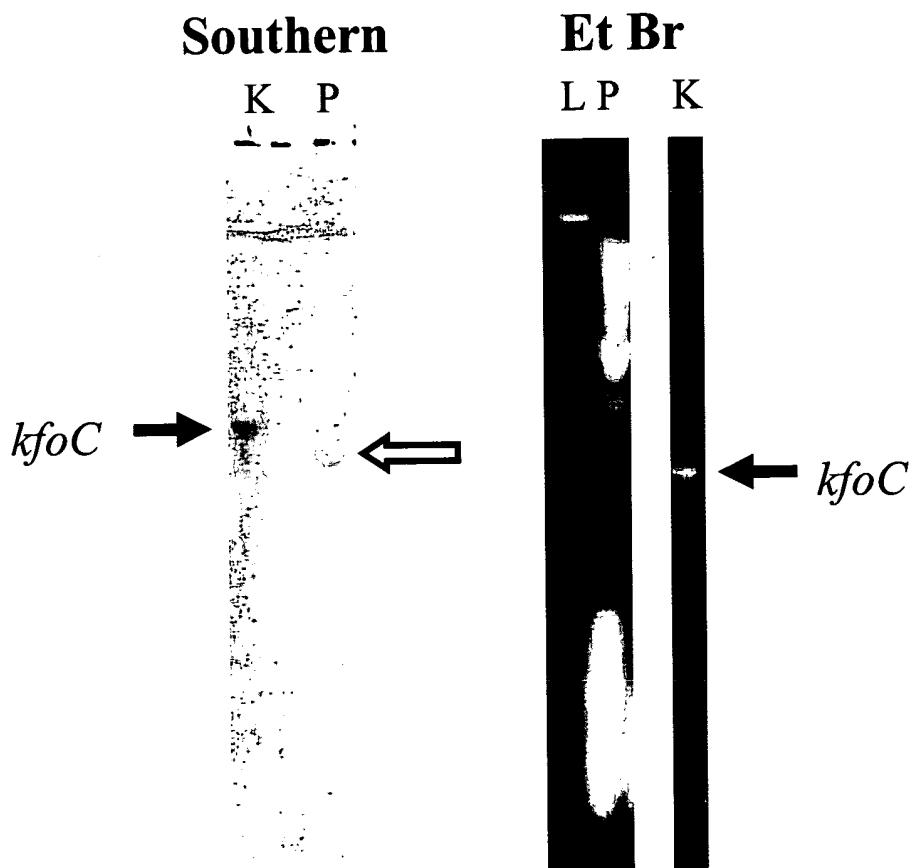
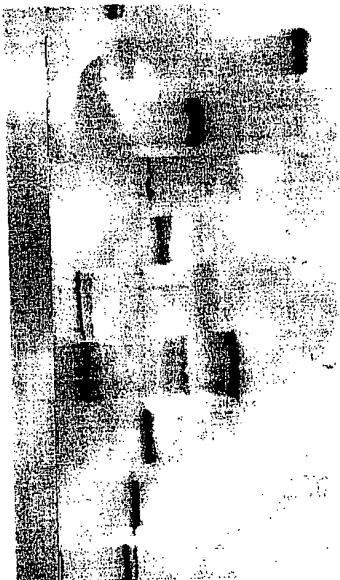


FIG. 8

Express Mail No.: EV272909140US Deposited: 08/15/2003  
Title: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY  
POLYMER GRAFTING AND METHODS OF MAKING AND USING  
SAME  
Inventors: Paul L. DeAngelis et al. Group: Unknown  
Filed: Herewith Examiner: Unknown  
Agent: Douglas J. Sorocco Dkt. No.: 3554.097  
SHEET 9 OF 41 Formal Drawings

Figure 9



**Figure 10**

A

pmHAS 972

703 mmHAS<sup>1-703</sup>

Domain A2

D247049 D527/529

2

A1 SIVTTENRPAILSTTLACLVNQKTHYPFEVIVTD  
A2 SIYIPAYNCANYIQRCVDSALNQ-TTVDILEVCICN

A1 DGSQEDLSPIRQYENKLDIRYVRQDNGFQASAAR  
A2 DGSQEDLSPIRQYENKLDIRYVRQDNGFQASAAR

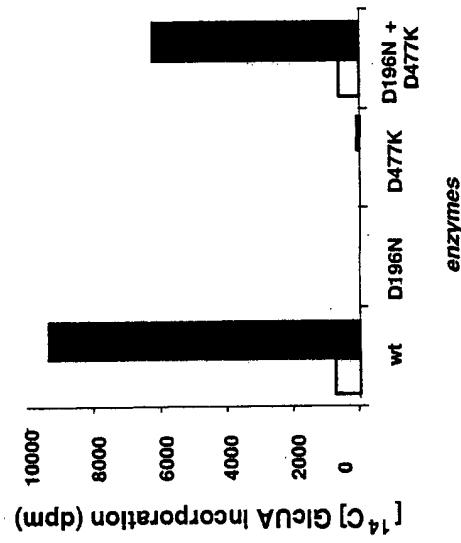
D2471249

A1 MGRLRALKDFIGLDCMAPNPLWHSYVAELLED  
A2 WDAVSEAVCWTQIQLSDNDTFRDQVETCVLVEFV  
E11 \* \* \*

DECA / 539

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SEARCHED \_\_\_\_\_ FILED \_\_\_\_\_ DECEMBER 10 2003  
U.S. PATENT AND TRADEMARK OFFICE  
10 OF 41

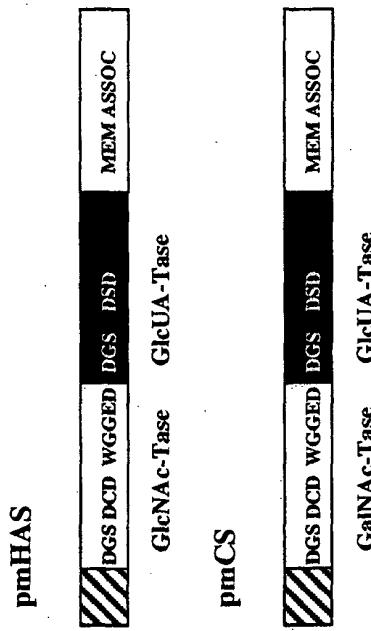
Figure 11



## Figure 12

|               |   |
|---------------|---|
| pmCS<br>pmHAS | 1. MNTLSQATKA YNSNDYELAL KLFTEKSAETY GRKIVEFGII ECKEKLSTNS<br><span style="float: right;">50</span><br><span style="float: right;">Q-----I-----T-----AMP</span>                                   |
|               | 51. IVS----- HDEKKNSVCD SLDITATOLLE SNVRKLTSE SERNSIAKNRW<br><span style="float: right;">100</span><br><span style="float: right;">S-NSAHTSVN KEEVN P-----V-B-----T</span>                        |
|               | 101. KSITGRKSEN AEIRKVELVP KDFPKDENVLA FLDGDHVNDFT WYGNRKKRSEG<br><span style="float: right;">150</span><br><span style="float: right;">-LL-E-----V-A-A-----K-----R--</span>                      |
|               | 151. IKPVVNKNIGL SILLPTENRS RILDITIACL VNQKTNYPFE VVVADDGSKE<br><span style="float: right;">200</span><br><span style="float: right;">---EHQHIV---VT-----P A-S-----H-----I-T-----Q</span>         |
|               | 201. NELETIVORVE CKLDIKYVRO KDKGYOLCAV RNGLGLRTAKY DFVSILDCDM<br><span style="float: right;">250</span><br><span style="float: right;">D-SP-IRQ---N---R---N-F-RS-A---M---L---IGI-----</span>      |
|               | 251. APGQLWVHSY LTEELIEDNDI VLIGDRKRYD THNITTAEQJL NDFPYLIESLP<br><span style="float: right;">300</span><br><span style="float: right;">---NP-----VA-----D-L TI-----I-QH-DEKD---MAS-L-----</span> |
|               | 301. ETATNNNPSI TSKGNISLDW RLEHFKKTDN IRIICDSPPFY FVAGNVAFSK<br><span style="float: right;">350</span><br><span style="float: right;">-VK---SVAA EGE-TV---Q-E-----S-----T-----A-----X</span>      |
|               | 351. EWLINKVGWFD KEFRHWGGED VEGYTRLEAK GCERFRVIDGG MATHQEPPGK<br><span style="float: right;">400</span><br><span style="float: right;">K-----S-F-----R-----S-----XT-----I-----Y-----</span>       |
|               | 401. ENETTEREAKK SITLKIVREK VPVITYRHLF LEDSHIHRIP LVSIYIPAYN<br><span style="float: right;">450</span><br><span style="float: right;">---D-----N---D-MR---N-V-----</span>                         |
|               | 451. CANYIQRCVD SALNQTUVDL EVCICNDGST DNTLEVINKL YGNNNPRVRIM<br><span style="float: right;">500</span><br><span style="float: right;">-----</span>  |
|               | 501. SKPNNGGIASA SNAAVSTAKG YYIGQLSDDD YLEPDAVELC EREFLKDCTL<br><span style="float: right;">550</span><br><span style="float: right;">-----</span>  |
|               | 551. ACVYTTTNRNV NPDGSЛИANG YNWPEFSREK LTITAMIAHHT RMFTTIRANWL<br><span style="float: right;">600</span><br><span style="float: right;">-----</span>  |
|               | 601. TDGFNMENIEN AVDYOMFLKL SEVGKPKHLN KICYNRVLHG DNTSIKKLG<br><span style="float: right;">650</span><br><span style="float: right;">-----K-----</span>   |
|               | 651. QXGNHIVVVN QSLMRQGINY YNYDKEDDID ESRKYIFNKT AEYQEMDML<br><span style="float: right;">700</span><br><span style="float: right;">-----T-----E-----I-----I-----</span>                          |
|               | 701. KDLKLQJQKD AKIAVSIFYP NTINGLVKKL NMNIEYNKNI FVIIILHVDKN<br><span style="float: right;">750</span><br><span style="float: right;">-----I-----V-----</span>                                    |
|               | 751. HLTRDIKEI LAFYHKHQVN ILLNNDISYY TSNRLIKTEA HLSNINKLSD<br><span style="float: right;">800</span><br><span style="float: right;">-----</span>  |
|               | 801. LININCEYITF DNHDLSLFVN DSYAYMKYD VGMNESALTH DWIEKINAHP<br><span style="float: right;">850</span><br><span style="float: right;">-----</span>   |
|               | 851. PTKKLIKTYF NDNDLRSMV KGASQGMIMK YALPHELLTI IKEVITSQG<br><span style="float: right;">900</span><br><span style="float: right;">-----K-----T-----A-----</span>                                 |
|               | 901. IDSVPEYNTK DIWFQFALLI LEKKTIGHVN KTSTLTYPW ERKLOWTNEQ<br><span style="float: right;">950</span><br><span style="float: right;">-----</span>  |
|               | 951. IOSARRGENI PVNKFIINSI TL<br><span style="float: right;">972</span><br><span style="float: right;">-----E-----R-----</span>   |

**Figure 13**



**Figure 14**

Express Mail No.: EV272909140US Deposited: 08/15/2003  
Title: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY  
POLYMER GRAFTING AND METHODS OF MAKING AND USING  
SAME

Inventors: Paul L. DeAngelis et al. Group: Unknown  
Filed: Herewith Examiner: Unknown  
Agent: Douglas J. Sorocco Dkt. No.: 3554.097  
SHEET 14 OF 41 Formal Drawings

91 APPLYSIIMTSHNTKEASINSLLQTYNNLEVIVVDDYSTSTDKTFQIA  
GKDLVSIIMSVFNSEDTIAYSLHSLLNQTYENIEILVCDCCSSDKSLEII  
..LVSIIIM\*..N\*E..I..S..SLL.QTY#N.E!..V..DD..S\*DK\*.#I.  
HS1 Kf1C con 140

141 SRIANSTSKVRTFRILNSNLGTYFAKNTGILKSKGDIIFFQDSSDVCHHER  
KSIAYSSSSRVRKVYSSSRKNQGPYNNIRNELLKAHGNFIFTQADDLISHPER  
..IA.S\*S\*VK.%...N.G;Y...N..I.K..G#.I.FQD.DD..H.ER  
HS1 Kf1C con 190

191 IERCVNALISNKDNIAVRCAYSRINLETQNIKVNDNKYKLGTLITLGVYR  
IQRQVEVLRNNKAVICM.ANWRVASNGKIOFFYDDKATRMSVSSMIKK  
I#R.V#.L..NK..I.....R!.#D....\*\$...!\*...!.\*.  
HS1 Kf1C con 240

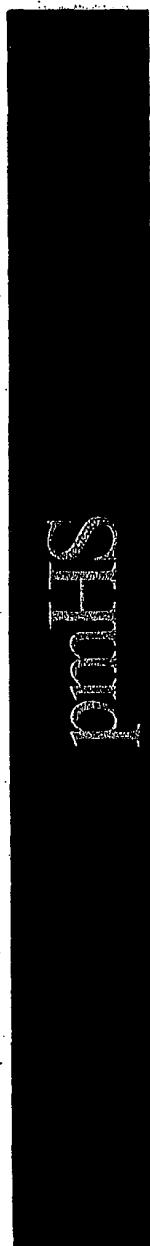
441 YITCDDDIRYPADYINTMIKKINKYND.KAAIGLHGVIFPSRVNKYFSSD  
IVLTDDDIYPPDYVEKMLNFYNSFAIFNCIVGIHGCIYIDAFDGD.QSK  
.!.DDDI.YP.DY!#.M....N.%....!G.HG.I%....#.S.  
HS2 Kf1A con 491

491 RIVYNFOKTFRKDTAVNILGTGTVAFRVSIFNKFSLSDFEHPGMVDIYFS  
RKVFSFTQGLLRPRVWNQLGTGTVFLRAQDQLPSLRYMDGSQR.FVDVRF  
R.V%..F.....\*...VN.LGTGTV...\*.....D.....VD!.FS  
HS2 Kf1A con 540

Figure 14 cont'd

617

1



**Figure 15A**

**Figure 15B**

|                                       |   |
|---------------------------------------|---|
| pmHS<br>pg1R<br>DcbF<br><br>Consensus | 1      10      20      30      40      50      60      70<br><hr/> MSLFKRATELFKSGNYKDALTLYENIARIYG—SESLVKYNIDI<br>MKRKKEMTQKQMTKNPPQHEKENELNTFQNKIDSLSKTTLNKDIISQQTLAKQDSKHPLSASLENEKLL<br>MSLFKRATELFKSGNYKDALTLYENIARIYG—SESLVKYNIDI<br>\$slFkrat#lfKsgnyKDaltlyeniARIyg...SeSlVkyNidi  |
| pmHS<br>pg1R<br>DcbF<br><br>Consensus | 71      80      90      100      110      120      130      140<br><hr/> CKK-NITQSNSKIEEDNISGENKF—SVSIKOLYNEISSELGITKERLGRAPPLVSIIMTSHNTEK<br>LKQLQLVLQEFEKIYTQNQALEKLEDKQTTSITOLYNEVAKSDLBLVKETNSVNPLVSIIIMTSHNTRQ<br>CKK-NITQSNSKIEEDNISGENEF—SVSIKOLYNEISSELGITKERLGRAPPLVSIIMTSHNTEK<br>cKk.#itqsk#KIEedNisgEnkf....svSIkOLYNEIsnS#LGItKEr-leapPLYSIIMTSHNTEk                         |
| pmHS<br>pg1R<br>DcbF<br><br>Consensus | 141      150      160      170      180      190      200      210<br><hr/> FIERASINSLLLQTYNNLEVIVVDDYSTDKTFQIASRIANSTSASKTFRRLNSNLGTYFAKNTGILSKKGDI<br>FIERASINSLLLQTYNNLEVIVVDDYSTDKTFQIASRIANSTSASKTFRRLNSNLGTYFAKNTGILSKKGDI<br>FIERASINSLLLQTYNNLEVIVVDDYSTDKTFQIASRIANSTSASKTFRRLNSNLGTYFAKNTGILSKKGDI<br>FIERASINSLLLQTYnNIEIIIIVDDYSTDKTFQIASRIAnSTSASKTFRRLNSNLGTYFAKNTGILSKKGDI |
| pmHS<br>pg1R<br>DcbF<br><br>Consensus | 211      220      230      240      250      260      270      280<br><hr/> IFFQDSDDVCHHERIERCVCNALLSNKDNIAVRCAYSRINLETQNCOKVNDNQYKLGILITLGvYRKVFNEI<br>IFFQDSDDVCHHERIERCVCNILLANKETIAVRCAYSRILAPETQHOCOKVNNMDYRLGFITLGHHRKVFQEI<br>IFFQDSDDVCHHERIERCVCNALLSNKDNIAVRCAYSRINLETQNCOKVNDNQYKLGILITLGvYRKVFNEI<br>IFFQDSDDVCHHERIERCVCNAll#nAVRCAYSRinLETQnIICKVn#nkykLB1ITLGvYRKVF#EI     |
| pmHS<br>pg1R<br>DcbF<br><br>Consensus | 281      290      300      310      320      330      340      350<br><hr/> GFFNCTTKASODEFYHRIIKYYGKRNINNLFPLIYNTMREDSLFSOMVEWVDENNICKTSORRONYLH<br>GFFNCTTKGSODEFFHRIAKYYGKEKIKHLLLPLIYNTMRENSLTDMVEWHDNNICQMSDTROHYAT<br>GFFNCTTKASODEFYHRIIKYYGKRNINNLFPLIYNTMREDSLFSOMVEWVDENNICKTSORRONYLH<br>GFFNCTTKAsSODEFXHRIIKYYGK#-InMLfLPLIYNTMRE#SLF#DMVEWID#nD#Qk#SDaRQnY1h                 |
| pmHS<br>pg1R<br>DcbF<br><br>Consensus | 351      360      370      380      390      400      410      420<br><hr/> EFQKJHNERKLNELKEIIPSPRIHDALPISKEMSKLSNPKIPVYINICSIPIPSRIKOLQYTIGVLKNQCDH<br>LFQRMHNETRASHDFKNLFQFPRIYDLPVPQEMSKLSNPKIPVYINICSIPIPSRIKOLRIGILKNQCDH<br>EFQKJHNERKFNELKEIIPSPRIHDALPISKEMSKLSNPKIPVYINICSIPIPSRIKOLQYTIGVLKNQCDH<br>eFOkLJHNERk#1K#I#F&FPRIHDALP I&kEMSKLSNPKIPVYINICSIPIPSRIKOLqytIGVLKNQCDH   |
| pmHS<br>pg1R<br>DcbF<br><br>Consensus | 421      430      440      450      460      470      480      490<br><hr/> FHIVLDGYPEVPDFIFIKKLGKATVINCQKNEStRDNGKFILLEKLIKENKDGYYITCDDDIRYPADYTN<br>FHIVLDGYPEVPDFIFIKKLGKATVINCQKNEStRDNGKFILLEELEKTDQDGYYITCDDDIYPSDYIN<br>FHIVLDGYPEVPDFIFIKKLGKATVINCQKNEStRDNGKFILLEKLIKENKDGYYITCDDDIRYPADYIN<br>FHIVLDGYPEVPDFIFIKKLGKATV!nCq#K#StRDNGKFILLEkLikeNxDGYYITCDDDIYPSDYin            |
| pmHS<br>pg1R<br>DcbF<br><br>Consensus | 491      500      510      520      530      540      550      560<br><hr/> THQKKKINKYMDKRAIGLHGVIFFPSRVNKYFSSDRIVYHNFQKPLENDTAVNlLGTGTvFRvSIFNKFSLs<br>THQKKLNEYDOKRIVIGLHGIIIPPSRvNKYFSSDRIVYHNFQKTFRK<br>THQKKKINKYMDKRAIGLHGVIFFPSRVNKYFSSDRIVYHNFQKTFRK<br>THQKKLNEYDOKRAGLNG!iFFPSRvnKYFSSDRIVYHNFQKPLEkd.avn.lgtgtv.frvs.bn.fslz   |
| pmHS<br>pg1R<br>DcbF<br><br>Consensus | 561      570      580      590      600      610      620      630<br><hr/> DFEHPGMVDOIYFSILCKKKNIlQvCISRPvNAlTEDNkNTETLFHEFQNRDTeIQSKLITSSNPvHGYSSIY<br>DFTHSGMADIYFSILCKKKNIlQvCISRPvNAlTEDNkROSETLYHQYRDNDEQQTQLIMENGvHGYSSIY  |
| pmHS<br>pg1R<br>DcbF<br><br>Consensus | 631      640      651<br><hr/> df.h.gn.diyfs.lckkknIlq.cisrp.nultedn...etl.h.....de.q..li...n.pugyzsziy<br>PLLNNNANySELIPCLSFYNE<br>PLVKNHPKFTDILPCLPFYFL   |

## Figure 15C

Multalin version 5.4.1

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Published research using this software should cite.

Multiple sequence alignment with hierarchical clustering

F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890

Symbol comparison table: blosum62

Gap weight: 12

Gap length weight: 2

Consensus levels: high=90% low=50%

Consensus symbols:

! is anyone of IV

\$ is anyone of LM

\* is anyone of FY

# is anyone of NDQEBZ

|                 |     |        |     |        |      |         |      |
|-----------------|-----|--------|-----|--------|------|---------|------|
| MSF:            | 651 | Check: | 0   | .      | .    |         |      |
| Name: A         |     | Len:   | 651 | Check: | 612  | Weight: | 0.58 |
| Name: B         |     | Len:   | 651 | Check: | 249  | Weight: | 0.58 |
| Name: pg1A      |     | Len:   | 651 | Check: | 7677 | Weight: | 1.08 |
| Name: DcbF      |     | Len:   | 651 | Check: | 7537 | Weight: | 1.76 |
| Name: Consensus |     | Len:   | 651 | Check: | 5816 | Weight: | 0.00 |

//

|           |  |                               |
|-----------|--|-------------------------------|
|           | 1  | 50                            |
| A2        | .....  | MSLFKR ATELFKSGNY KDALTLYENI  |
| B10       | .....  | MSLFKR ATELFKSGNY KDALTLYENI  |
| pg1A      | MKRKKEMTQK QMTKNPPQHE KENEINTFQN KIDSLLKTTLN KDIISQQTILL |                               |
| DcbF      | .....  | MSLFKR ATELFKSGNY KDALTLYENI  |
| Consensus | .....  | \$s1fkr at#lfKsgny KDaltlyeni |
|           | 51   | 100                           |
| A2        | AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENKF....    |                               |
| B10       | AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENKF....    |                               |
| pg1A      | AKQDSKHPLS ASLENENKLL LKQLQLVLQE FEKIYTYNQA LEAKLEKDKQ   |                               |
| DcbF      | AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENEF....    |                               |
| Consensus | AKIyg....S eSLvkyNidi cKk.#itqsk s#KieedNis gEnkf....    |                               |
|           | 101  | 150                           |
| A2        | SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL   |                               |
| B10       | SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL   |                               |
| pg1A      | TTSITDLYNE VAKSDLGLVK ETNSVNPLVS IIMTSHNTAQ FIEASINSLL   |                               |
| DcbF      | SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL   |                               |
| Consensus | svSIkDLYNE !snS#LGitK ErlgapPLVs IIMTSHNTek FIEASINSLL   |                               |
|           | 151  | 200                           |
| A2        | LQTYNNLEVI VVDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTyFAKN   |                               |
| B10       | LQTYNNLEVI VVDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTyFAKN   |                               |
| pg1A      | LQTYKNIEII IVDDDSSDNT FEIASRIANT TSKVRVFRNL SNLGTyFAKN   |                               |
| DcbF      | LQTYNNLEVI VVDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTyFAKN   |                               |
| Consensus | LQTyNnIE! !VDDyStDkt F#IASRIANs TSKVktFRNL SNLGTyFAKN    |                               |

### Fig. 15C cont'd

|  |     |
|--|-----|
| 201  | 250 |
| A2 TGILKSKGDI IFFQDSDVC HHERIERCVN ALLSNKDNIA VRCAYSRINL         |     |
| B10 TGILKSKGDI IFFQDSDVC HHERIERCVN ALLSNKDNIA VRCAYSRINL        |     |
| pg1A TGILKSKGDI IFFQDSDVC HHERIERCVN ILLANKETIA VRCAYSRLAP       |     |
| DcbF TGILKSKGDI IFFQDSDVC HHERIERCVN ALLSNKDNIA VRCAYSRINL       |     |
| Consensus TGILKSKGDI IFFQDSDVC HHERIERCVN aLLsNK#nIA VRCAYSRIn1  |     |
|  |     |
| 251  | 300 |
| A2 ETQNIIKVND NKYKLGLITL GVYRKVFNEI GFFNCTTKAS DDEFYHRIIK        |     |
| B10 ETQNIIKVND NKYKLGLITL GVYRKVFNEI GFFNCTTKAS DDEFYHRIIK       |     |
| pg1A ETOHIIKVNN MDYRLGFITL GMHRKVFQEI GFFNCTTKGS DDEFFHRIAK      |     |
| DcbF ETONIIKVND NKYKLGLITL GVYRKVFNEI GFFNCTTKAS DDEFYHRIIK      |     |
| Consensus ETQnIIKVN# nkYkLGltl GvYRKVF#EI GFFNCTTKaS DDEFYHRIIK  |     |
|  |     |
| 301  | 350 |
| A2 YYGKNRINNL FPLYYNTMR EDSLFSMDMVE WVDENNIKQK TSDARQNYLH        |     |
| B10 YYGKNRINNL FPLYYNTMR EDSLFSMDMVE WVDENNIKQK TSDARQNYLH       |     |
| pg1A YYGKEKIKNL LLPLOYNTMR ENSLFTDMVE WIDNHNIIQK MSDTRQHYAT      |     |
| DcbF YYGKNRINNL FPLYYNTMR EDSLFSMDMVE WVDENNIKQK TSDARQNYLH      |     |
| Consensus YYGK#rInNL FPLYYNTMR E#SLFSMDMVE W!D#nNIKQK tSDaRQnYlh |     |
|  |     |
| 351  | 400 |
| A2 EFQKIHNERK LNELKEIFSF PRIHDALPIS KEMSKLSNPK IPVYINICSI        |     |
| B10 EFQKIHNERK LNELKEIFSF PRIHDALPIS KEMSKLSNPK IPVYINICSI       |     |
| pg1A LFQAMHNETA SHDFKNLFQF PRIYDALPVP QEMSKLSNPK IPVYINICSI      |     |
| DcbF EFQKIHNERK FNELKEIFSF PRIHDALPIS KEMSKLSNPK IPVYINICSI      |     |
| Consensus eFQkiHNerK .n#LK#iFsF PRIHDALP!s KEMSKLSNPK IPVYINICSI |     |
|  |     |
| 401  | 450 |
| A2 PSRIKQLQYT IGVLKNCQDH FHIYLDGYPE VPDFIKKLGN KATVINCNQK        |     |
| B10 PSRIKQLQYT IGVLKNCQDH FHIYLDGYPE VPDFIKKLGN KATVINCNQK       |     |
| pg1A PSRIAQLRRRI IGIKNOCQDH FHIYLDGYVE IPDFIKNLGN KATVVKCKDK     |     |
| DcbF PSRIKQLQYT IGVLKNCQDH FHIYLDGYPE VPDFIKKLGN KATVINCNQK      |     |
| Consensus PSRIKQLqyt IG!LKNQCDH FHIYLDGYpE !PDFIKKLGN KATV!nCq#K |     |
|  |     |
| 451  | 500 |
| A2 NESIRDNGKF ILLEKLIKEN KDGYYITCDD DIRYPADYTN TMIKKINKYN        |     |
| B10 NESIRDNGKF ILLEKLIKEN KDGYYITCDD DIRYPADYIN TMIKKINKYN       |     |
| pg1A DNSIRDNGKF ILLEKLIKEN QDGYYITCDD DIIYPSDYIN TMIKKLNeyD      |     |
| DcbF NESIRDNGKF ILLEKLIKEN KDGYYITCDD DIRYPADYIN TMIKKINKYN      |     |
| Consensus ##SIRDNGKF ILLEkLIken KDGYYITCDD DIRYPADYIN TMIKKLNky# |     |
|  |     |
| 501  | 550 |
| A2 DKAAIGLHGv IFPSRVNKyF SSDRIVYNFQ KPLENDTAVN ILGTGTVAFR        |     |
| B10 DKAAIGLHGv IFPSRVNKyF SSDRIVYNFQ KPLENDTAVN ILGTGTVAFR       |     |
| pg1A DKAVIGLHG1 LFPSRMTKYF SADRIVSYFY KPLEKDkAVN VLGTGTVsFR      |     |
| DcbF DKAAIGLHGv IFPSRVNKyF SSDRIVYNFQ KTFRK.....                 |     |
| Consensus DKAAIGLHG! IFPSRVnKyF SsDRivYnFq Kplekd.avn .lgtgtv.fr |     |
|  |     |
| 551  | 600 |
| A2 VSIFNKFSLs DFEHPGMVDI YFSILCKKNN ILQVCISRPS NWLTEDNkNT        |     |
| B10 VSIFNKFSLs DFEHPGMVDI YFSILCKKNN ILQVCISRPS NWLTEDNkNT       |     |
| pg1A VSLFNQFSLS DFTHSGMADI YFSLLCKKNN ILQICISRPA NWLTEDNRDS      |     |
| DcbF .....   |     |
| Consensus vs.fn.fs1s df.h.gm.di yfs.lckknn ilq.cisrp. nwltedn... |     |

**Fig. 15C c nt'd**

|  |       |
|--|-------|
| 601  | 650   |
| A2 ETLFHEFQNR DEIQSKLIIS NNPGYSSIIY PLLNNNANYS ELIPCLSFYN      |       |
| B10 ETLFHEFQNR DEIQSKLIIS NNPGYSSIIY PLLNNNANYS ELIPCLSFYN     |       |
| pg1A ETLYHQYRDN DEQQTQLIME NGPVGYSSIIY PLVKNHPKFT DLIPCLPFYF   |       |
| DcbF .....   | ..... |
| Consensus etl.h.... de.q..li... n.pwgyssiy pl..n.... lipcl.fy. |       |
| 651  |       |
| A2 E   |       |
| B10 E  |       |
| pg1A L   |       |
| DcbF .   |       |
| Consensus .  |       |

## Figure 15D

Multalin version 5.4.1

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Published research using this software should cite

Multiple sequence alignment with hierarchical clustering

F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890

Symbol comparison table: blosum62

Gap weight: 12

Gap length weight: 2

Consensus levels: high=90% low=50%

Consensus symbols:

! is anyone of IV

\$ is anyone of LM

% is anyone of FY

# is anyone of NDQEBZ

MSF: 651 Check: 0

|                 |          |             |              |
|-----------------|----------|-------------|--------------|
| Name: pmHS      | Len: 651 | Check: 612  | Weight: 0.75 |
| Name: pglA      | Len: 651 | Check: 7677 | Weight: 0.75 |
| Name: DcbF      | Len: 651 | Check: 7537 | Weight: 1.49 |
| Name: Consensus | Len: 651 | Check: 5816 | Weight: 0.00 |

//

|           |   |                               |
|-----------|---|-------------------------------|
|           | 1   | 50                            |
| pmHS      | .....   | MSLFKR ATELFKSGNY KDALTLYENI  |
| pglA      | MKRKEMTQK QMTKNPPQHE KENELENFTQNE KIDSLLTTLN KDIISQQTLL |                               |
| DcbF      | .....   | MSLFKR ATELFKSGNY KDALTLYENI  |
| Consensus | .....   | \$s1fkr at#lfKsgny KDaltlyeni |
|           | 51  | 100                           |
| pmHS      | AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENKF....   |                               |
| pglA      | AKQDSKHPLS ASLENENKLL LKQLQLVLOE FEKIYTQNA LEAKLEKDKQ   |                               |
| DcbF      | AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENEF....   |                               |
| Consensus | AKiyg....S eSLvkyNidi cKk.#itqsk s#KieedNis gEnkf....   |                               |
|           | 101   | 150                           |
| pmHS      | SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSNTEK FIEASINSLL   |                               |
| pglA      | TTSITDLYNE VAKSDLGLVK ETNSVNPLVS IIMTSNNTAQ FIEASINSLL  |                               |
| DcbF      | SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSNTEK FIEASINSLL   |                               |
| Consensus | svSIKDLYNE !snS#LGitK ErlgapPLVS IIMTSNNTek FIEASINSLL  |                               |
|           | 151   | 200                           |
| pmHS      | LQTYNNLEVI VVDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN  |                               |
| pglA      | LQTYKNIEII IVDDDSSDNF FEIASRIANT TSKVRVFRNL SNLGTYFAKN  |                               |
| DcbF      | LQTYNNLEVI VVDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN  |                               |
| Consensus | LQTyNnE!I !VDDyStDkt F#IASRIANs TSKVktFRNL SNLGTYFAKN   |                               |
|           | 201   | 250                           |
| pmHS      | TGILKSKGDI IFFQDSDDVC HHERIERCVN ALLSNKDNIA VRCAYSRINL  |                               |
| pglA      | TGILKSKGDI IFFQDSDDVC HHERIERCVN ILLANKETIA VRCAYSRIAP  |                               |
| DcbF      | TGILKSKGDI IFFQDSDDVC HHERIERCVN ALLSNKDNIA VRCAYSRINL  |                               |
| Consensus | TGILKSKGDI IFFQDSDDVC HHERIERCVN aLLsNK#nIA VRCAYSRinl  |                               |
|           | 251   | 300                           |
| pmHS      | ETQNIIKVND NKYKLGLITL GVYRKVFNEI GFFNCTTKAS DDEFYHRIIK  |                               |
| pglA      | ETOIIIKVNN MDYRLGFITL GMHRKVQEI GFFNCTTKGS DDEFFHRIAK   |                               |
| DcbF      | ETQNIIKVND NKYKLGLITL GVYRKVFNEI GFFNCTTKAS DDEFYHRIIK  |                               |
| Consensus | ETQnIIKVn# nkYKLGlITL GvyRKVF#EI GFFNCTTKaS DDEF#HRIIK  |                               |

## Figure 15D

|           |   |  |     |
|-----------|---|--|-----|
|           | 301   |  | 350 |
| pmHS      | YYGKNRINNL FLPLYYNTMR EDSLFSMDMVE WVDENNIKQK TSDARQNYLH |  |     |
| pg1A      | YYGKEKIKNL LLPLYYNTMR ENSLFTDMVE WIDNHNIIQK MSDTRQHYAT  |  |     |
| DcbF      | YYGKNRINNL FLPLYYNTMR EDSLFSMDMVE WVDENNIKQK TSDARQNYLH |  |     |
| Consensus | YYGK#rInNL flPLYYNTMR E#SLFsDMVE W!D#nNIkQK tSDaRQnYh   |  |     |
|           | 351   |  | 400 |
| pmHS      | EFOKIHNERK LNELKEIFSF PRIHDALPIS KEMSKLSNPK IPVYINICSI  |  |     |
| pg1A      | LFQAMHNETA SHDFKNLFQF PRIYDALPVP QEMSKLSNPK IPVYINICSI  |  |     |
| DcbF      | EFOKIHNERK FNELKEIFSF PRIHDALPIS KEMSKLSNPK IPVYINICSI  |  |     |
| Consensus | eFQkiHNERk .n#lK#iFsF PRIhDALP!s KEMSKLSNPK IPVYINICSI  |  |     |
|           | 401   |  | 450 |
| pmHS      | PSRIKQLQYT IGVLKNQCDH FHIYLDGYPE VPDFIKKLGN KATVINCQNK  |  |     |
| pg1A      | PSRIAQLRRRI IGILKNQCDH FHIYLDGYVE IPDFIKNLGN KATVVHCKDK |  |     |
| DcbF      | PSRIKQLQYT IGVLKNQCDH FHIYLDGYPE VPDFIKKLGN KATVINCQNK  |  |     |
| Consensus | PSRIKQLqyt IG!LKNQCDH FHIYLDGYpE !PDFIKkLGN KATV!nCq#K  |  |     |
|           | 451   |  | 500 |
| pmHS      | NESIRDNGKF ILLEKLIKEN KDGYYITCDD DIRYPADYTN TMIKKINKYN  |  |     |
| pg1A      | DNSIRDNGKF ILLEELIEKN QDGYYITCDD DIIYPSDYIN TMIKKLNNEYD |  |     |
| DcbF      | NESIRDNGKF ILLEKLIKEN KDGYYITCDD DIRYPADYIN TMIKKINKYN  |  |     |
| Consensus | ##SIRDNGKF ILLEkLIken xDGYYITCDD DIRYPADYin TMIKKINKY#  |  |     |
|           | 501   |  | 550 |
| pmHS      | DKAAIGLHGv IFPSRVNKyF SSDRIVYNFQ KPLENDTAVN ILGTGTVAFR  |  |     |
| pg1A      | DKAVIGLHGv LFPSRMTKYF SADRlVYSFY KPLEKDKAVN VLGTGTVSFR  |  |     |
| DcbF      | DKAAIGLHGv IFPSRVNKyF SSDRIVYNFQ KTFRK.....             |  |     |
| Consensus | DKAaIGLHG! iFPSRvnKYF SsDRiVYnFq Kplekd.avn .lgtgtv.fr  |  |     |
|           | 551   |  | 600 |
| pmHS      | V\$IFNKFSLS DFEHPGMVDI YFSILCKKNN ILQVCISRPS NWLTEDNKNT |  |     |
| pg1A      | VSLFNQFSLS DFTHSGMADI YFSLLCKKNN ILQICISRPA NWLTEDNRDS  |  |     |
| DcbF      | .....   |  |     |
| Consensus | vs.fn.fsIs df.h.gm:di yfs.lckknn ilq.cisrp. nwltedn...  |  |     |
|           | 601   |  | 650 |
| pmHS      | ETLFHEFQNR DEIQSKLIIS NNPWGYSSIY PLLNNNANYS ELIPCLSFYN  |  |     |
| pg1A      | ETLYHQYRDN DEQQTQLIME NGPWGYSSIY PLVKNHPKFT DLIPCLPFYF  |  |     |
| DcbF      | .....   |  |     |
| Consensus | etl.h..... de.q..li.. n.pwgysiy pl...n.... lipcl.fy.    |  |     |
|           | 651   |  |     |
| pmHS      | E   |  |     |
| pg1A      | L   |  |     |
| DcbF      | .   |  |     |
| Consensus | .   |  |     |

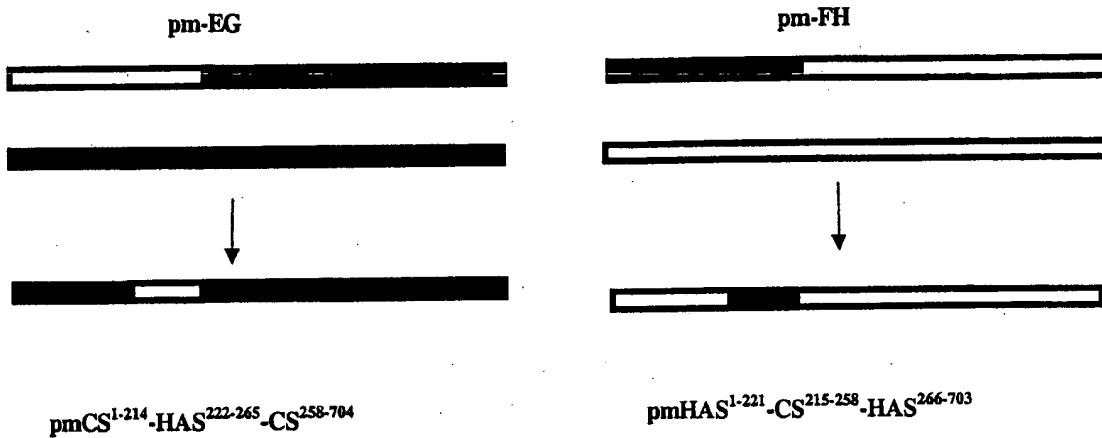
**Figure 16**

| enzyme      | activity   |
|-------------|------------|
| pmHAS 1-703 | HAS        |
| pmCS 1-704  | CS         |
| ↓           |            |
| pm-EG       | GlcUA-Tase |
| pm-FH       | CS         |
| ↓           |            |
| pm-IK       | GlcUA-Tase |
| pm-JL       | HAS        |

Figure 17

|                    | 211  | 220 | 230 | 240 | 250 |
|--------------------|--|-----|-----|-----|-----|
| P <sub>n</sub> HAS | NKLDIYRYRQKDNGFQASAARRNMLRLAKYDFIGLLDCDMI  |     |     |     |     |
| P <sub>n</sub> CS  | QKLDIYRYRQKDGYQLCAVRNLGLRTAKYDFYSILDCDMI   |     |     |     |     |
| Turkey             | EKLDIYRYRQKDGYQLCAVRNLGLRTAKYDFYSILDCDM    |     |     |     |     |
| Goose              | VDIKYYRQKDGYQLCAVRNLGLRTAKYDFYSILDC        |     |     |     |     |
| Sea-lion           | KYYRQKDGYQLCAVRNLGLRTAKYDFYSILDC           |     |     |     |     |
| Consensus          | ...dikYYRQKDyG%Q1cAvRN\$GLRtAKYDF!siLDC... |     |     |     |     |
| mutant 1           | ★  |     |     |     |     |
| mutant 2           |  | ★   |     |     |     |
| mutant 3           |  | ★   |     |     |     |
| mutant 4           | ★  | ★   |     |     |     |
| mutant 5           | ★  | ★   |     |     |     |
| mutant 6           |  | ★★  |     |     |     |
| mutant 7           | ★  | ★★  |     |     |     |
| mutant 8           |  |     |     |     | ★   |
| mutant 9           |  |     |     |     | ★★  |

## Figure 18



## Figure 19

| enzyme  | activity      |    |            |
|---------|---------------|----|------------|
|         | HAS           | CS | GlcUA-Tase |
| pm-BD   | -             | +  | [+]        |
| + pm-AC | +             | -  | [+]        |
| + pm-FH | -             | +  | +          |
| pm-EG   | -             | -  | +          |
| Pm-JL   | +             | -  | +          |
| pm-IK   | -             | -  | +          |
| pmCHC   | +             | +  | +          |
| pmHCH   | not expressed |    |            |

Express Mail No.: EV272909140US Deposited: 08/15/2003  
Title: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY  
POLYMER GRAFTING AND METHODS OF MAKING AND USING  
SAME  
Inventors: Paul L. DeAngelis et al. Group: Unknown  
Filed: Herewith Examiner: Unknown  
Agent: Douglas J. Sorocco Dkt. No.: 3554.097  
SHEET 27 OF 41 Formal Drawings

## FIGURE 20



## FIGURE 21

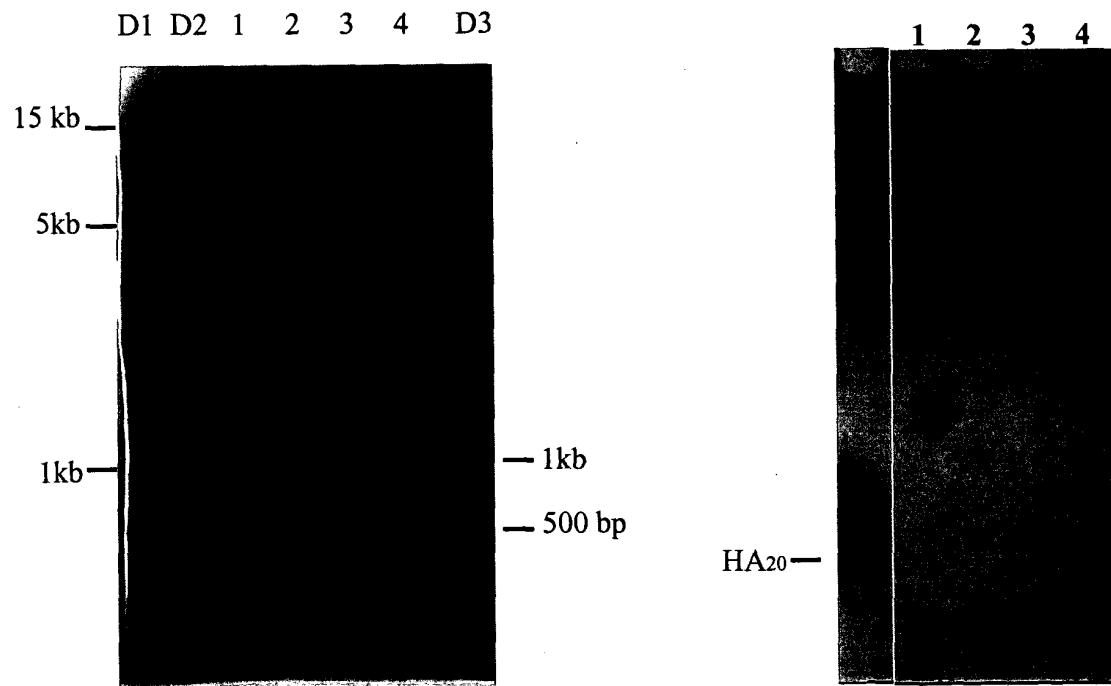


FIGURE 22.  
Model of *Pasteurella*  
Synthase Polymerization

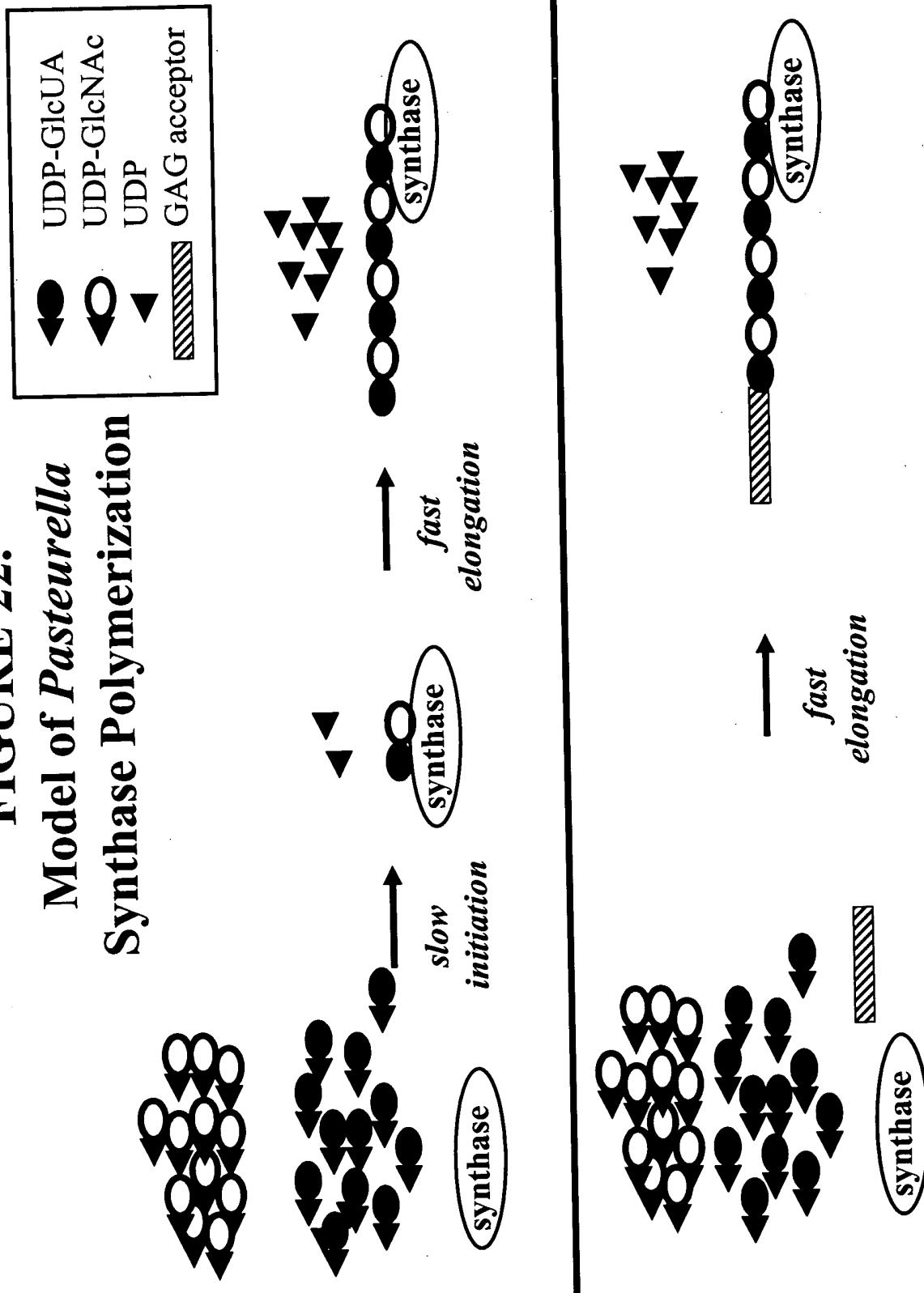


FIGURE 23.

Model of Reaction Synchronization

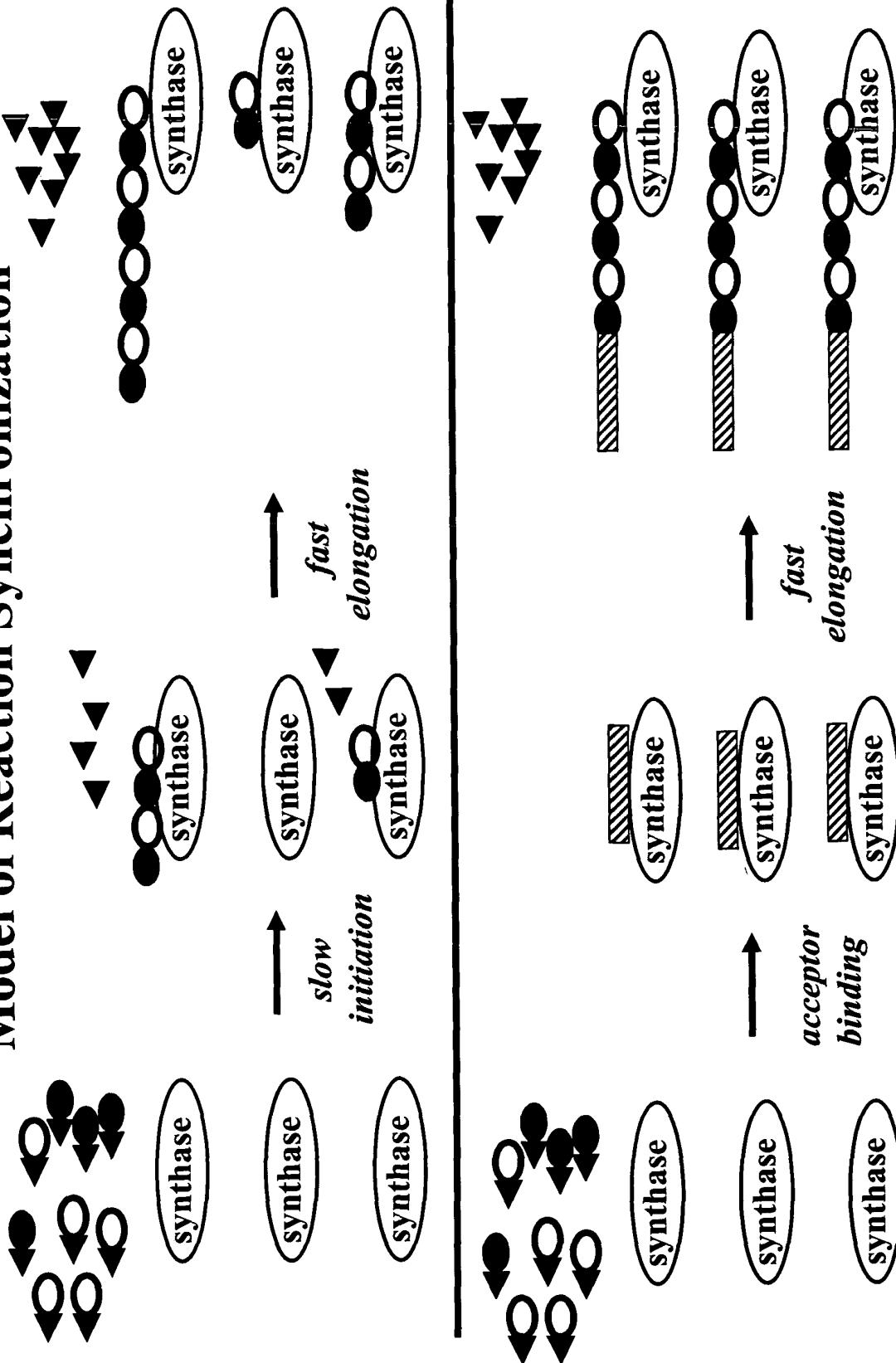
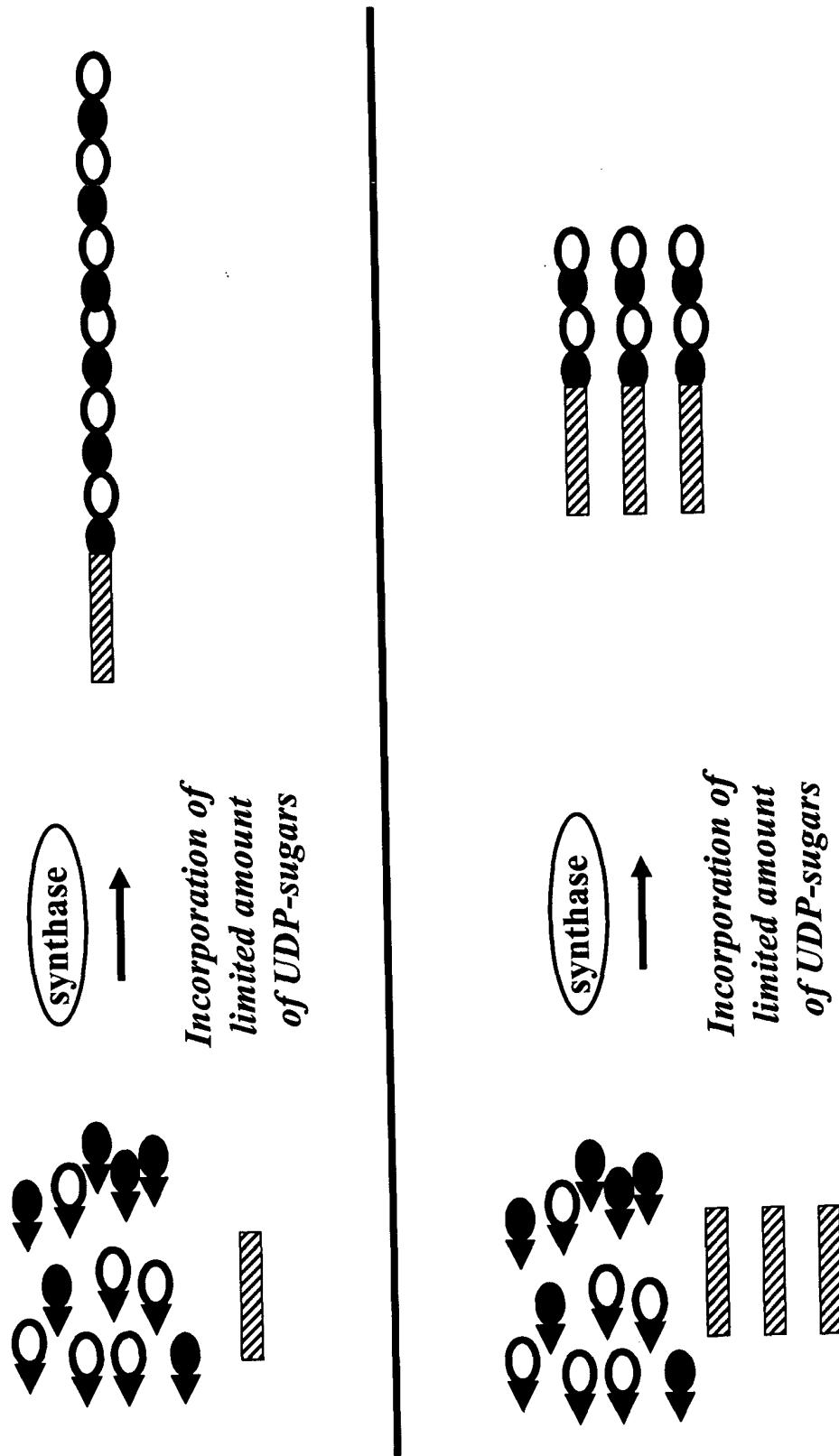


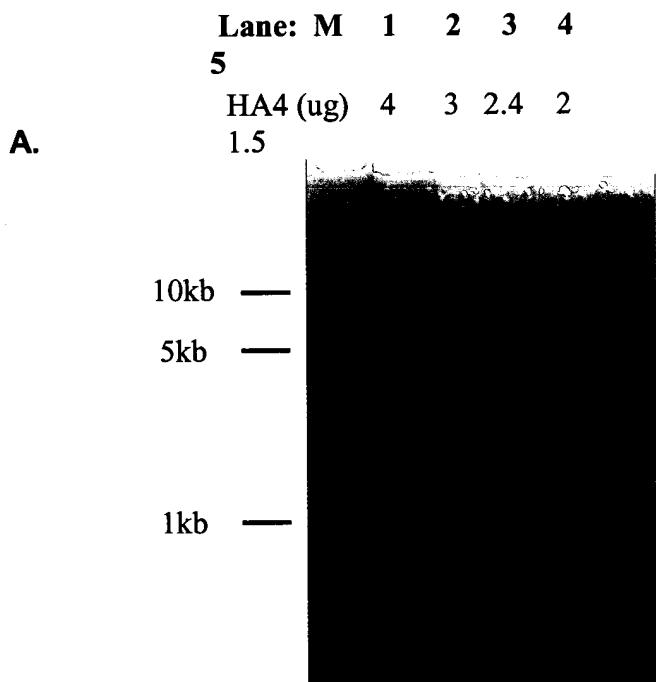
FIGURE 24.  
Model of Stoichiometric Control of Polymer Size



## FIGURE 25



## FIGURE 26

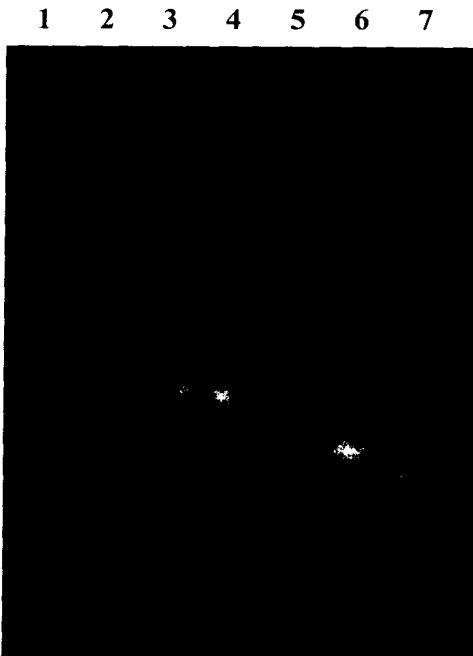


B.

| Sample No | Mn     | Mw     | polydispersity |
|-----------|--------|--------|----------------|
| #1        | 283400 | 283800 | 1.001          |
| #2        | 346400 | 347000 | 1.002          |
| #3        | 422200 | 423700 | 1.004          |
| #4        | 490000 | 493100 | 1.006          |
| #5        | 569700 | 575200 | 1.010          |

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Filed: Herewith Examiner: Unknown  
Agent: Douglas J. Sorocco Dkt. No.: 3554.097  
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## FIGURE 27



## FIGURE 28

572kDa HA ( $\mu$ g)

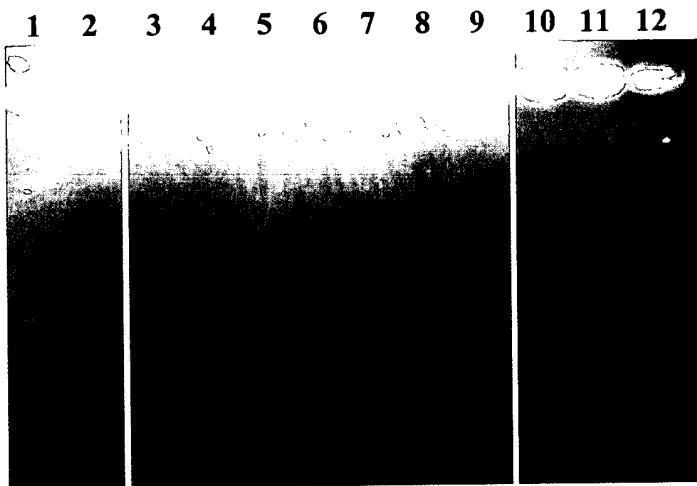
5 10 15

970kDa HA ( $\mu$ g)

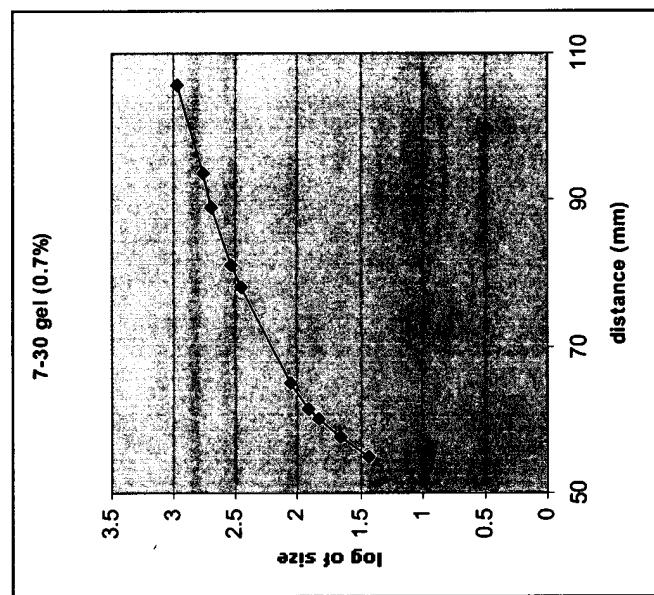
5 10 15

Genzyme HA ( $\mu$ g)

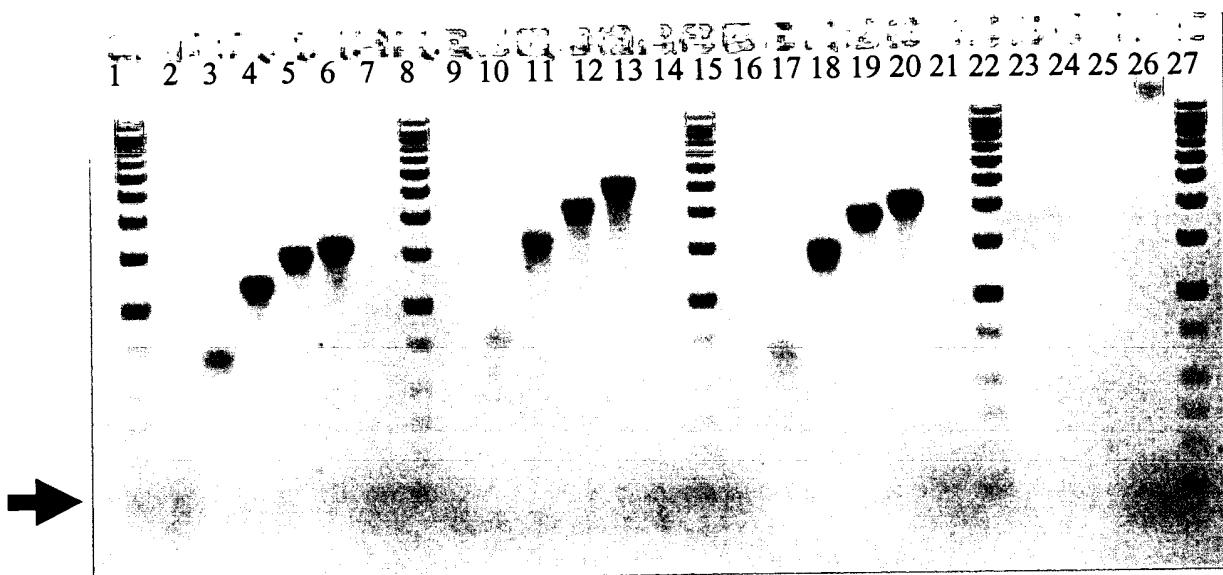
8



**FIGURE 29.**  
**Agarose Gels of Ladders and Migration**



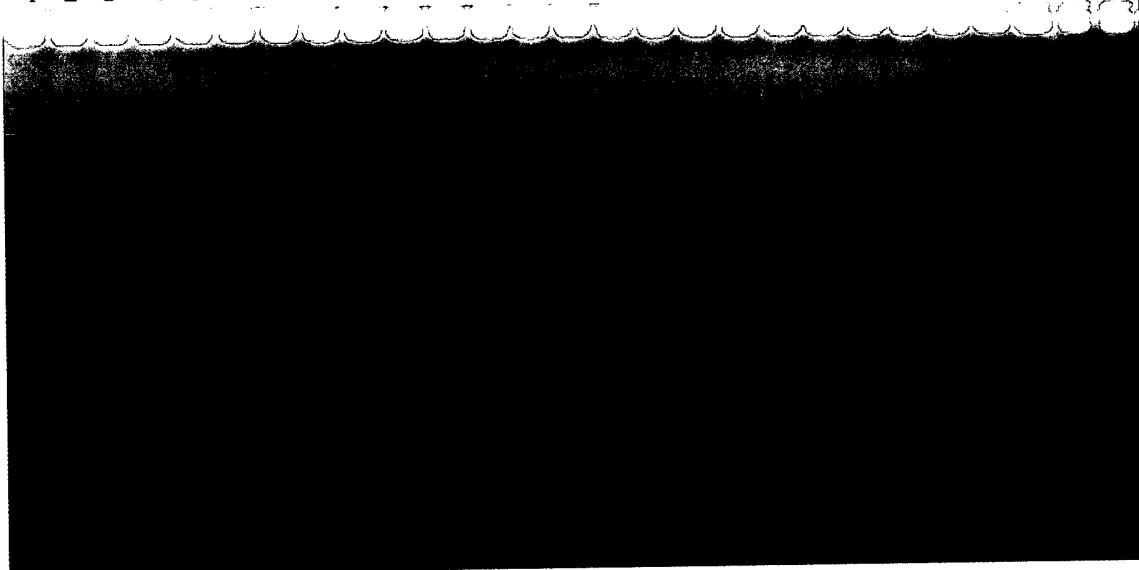
## FIGURE 30



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Filed: Herewith Examiner: Unknown  
Agent: Douglas J. Sorocco Dkt. No.: 3554.097  
SHEET 38 OF 41 Formal Drawings

## FIGURE 31

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26



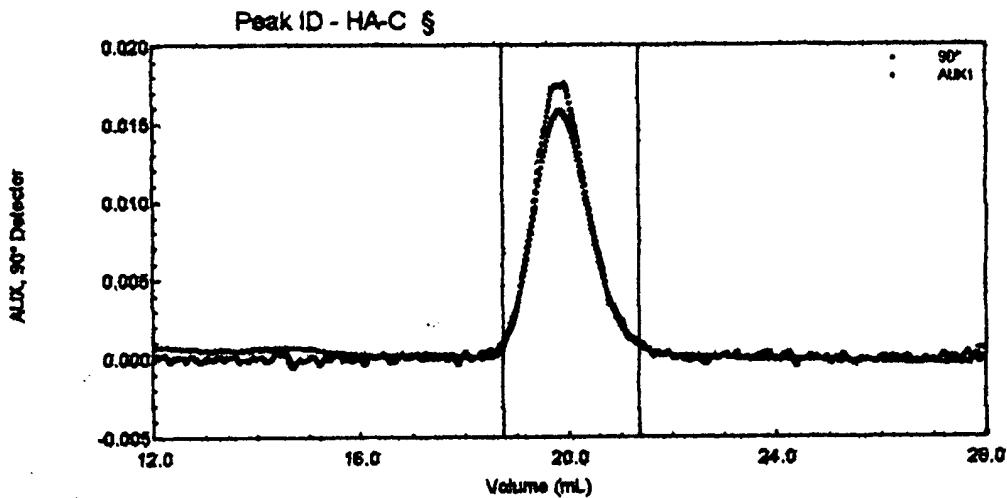
## FIGURE 32



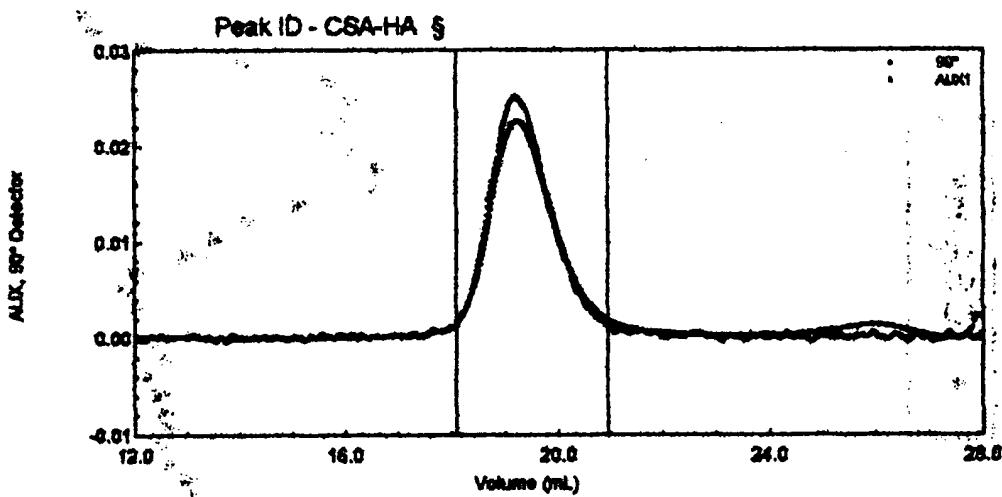
Time: 0 2 4 4 6 O/N 0  
Feeding round: - 1 2 1 3 3 -

## FIGURE 33

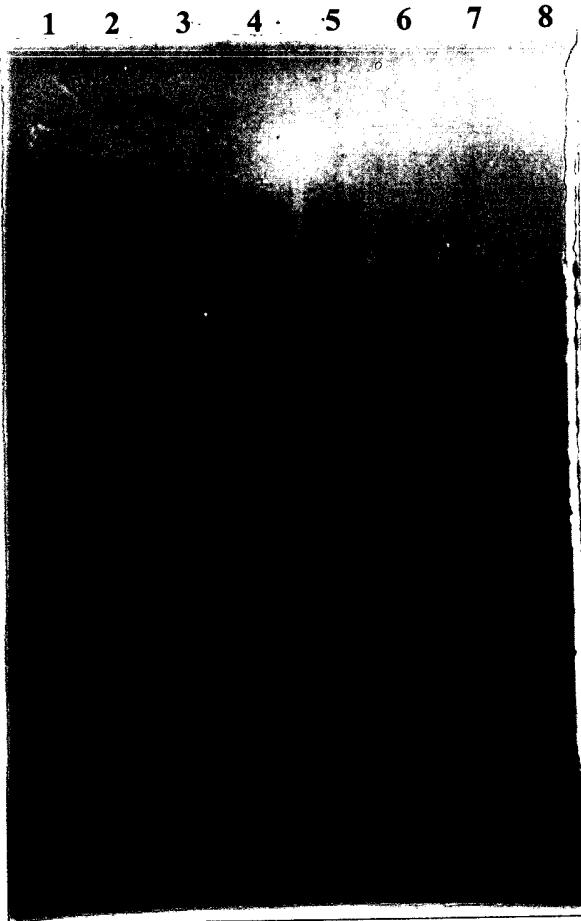
A.



B.



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POLYMER GRAFTING AND METHODS OF MAKING AND USING  
SAME  
Inventors: Paul L. DeAngelis et al. Group: Unknown  
Filed: Herewith Examiner: Unknown  
Agent: Douglas J. Sorocco Dkt. No.: 3554.097  
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**FIG. 34**